

Q.Nguyen

Page 1 of 7

H10

12-22-00

1632 P2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/462,517

DATE: 11/21/2000
TIME: 11:52:46

Input Set : A:\sequence
Output Set: N:\CRF3\11212000\I462517.raw

3 <110> APPLICANT: Aurora Biosciences Corporation
4 Zucker, Charles
5 Mendlein, John
6 Sun, Yumei
7 Tsunoda, Susan
8 Sierralta, Jimena
10 <120> TITLE OF INVENTION: Compositions And Methods For Identifying Modulators and Transducisomes
12 <130> FILE REFERENCE: AURO1210-1
14 <140> CURRENT APPLICATION NUMBER: 09/462,517
15 <141> CURRENT FILING DATE: 2000-05-18
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 674
23 <212> TYPE: PRT
24 <213> ORGANISM: Drosophila melanogaster
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31 Met Val Thr Leu Asp Lys Thr Gly Lys Ser Phe Gly Ile Cys Ile
32 20 25 30
34 Val Arg Gly Glu Val Lys Asp Ser Pro Asn Thr Lys Thr Thr Gly Ile
35 35 40 45
37 Phe Ile Lys Gly Ile Val Pro Asp Ser Pro Ala His Leu Cys Gly Arg
38 50 55 60
40 Leu Lys Val Gly Asp Arg Ile Leu Ser Leu Asn Gly Lys Asp Val Arg
41 65 70 75 80
43 Asn Ser Thr Glu Gln Ala Val Ile Asp Leu Ile Lys Glu Ala Asp Phe
44 85 90 95
46 Lys Ile Glu Leu Glu Ile Gln Thr Phe Asp Lys Ser Asp Glu Gln Gln
47 100 105 110
49 Ala Lys Ser Asp Pro Arg Ser Asn Gly Tyr Met Gln Ala Lys Asn Lys
50 115 120 125
52 Phe Asn Gln Glu Gln Thr Thr Asn Asn Ala Ser Gly Gly Gln Gly
53 130 135 140
55 Met Gly Gln Gly Gln Gly Gln Gly Met Ala Gly Met Asn Arg
56 145 150 155 160
58 Gln Gln Ser Met Gln Lys Arg Asn Thr Thr Phe Thr Ala Ser Met Arg
59 165 170 175
61 Gln Lys His Ser Asn Tyr Ala Asp Glu Asp Asp Glu Asp Thr Arg Asp
62 180 185 190
64 Met Thr Gly Arg Ile Arg Thr Glu Ala Gly Tyr Glu Ile Asp Arg Ala
65 195 200 205
67 Ser Ala Gly Asn Cys Lys Leu Asn Lys Gln Glu Lys Asp Arg Asp Lys
68 210 215 220
70 Glu Gln Glu Asp Glu Phe Gly Tyr Thr Met Ala Lys Ile Asn Lys Arg
71 225 230 235 240

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Input Set : A:\sequence
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73 Tyr Asn Met Met Lys Asp Leu Arg Arg Ile Glu Val Gln Arg Asp Ala
 74 245 250 255
 76 Ser Lys Pro Leu Gly Leu Ala Leu Ala Gly His Lys Asp Arg Gln Lys
 77 260 265 270
 79 Met Ala Cys Phe Val Ala Gly Val Asp Pro Asn Gly Ala Leu Gly Ser
 80 275 280 285
 82 Val Asp Ile Lys Pro Gly Asp Glu Ile Val Glu Val Asn Gly Asn Val
 83 290 295 300
 85 Leu Lys Asn Arg Cys His Leu Asn Ala Ser Ala Val Phe Lys Asn Val
 86 305 310 315 320
 88 Asp Gly Asp Lys Leu Val Met Ile Thr Ser Arg Arg Lys Pro Asn Asp
 89 325 330 335
 91 Glu Gly Met Cys Val Lys Pro Ile Lys Lys Phe Pro Thr Ala Ser Asp
 92 340 345 350
 94 Glu Thr Lys Phe Ile Phe Asp Gln Phe Pro Lys Ala Arg Thr Val Gln
 95 355 360 365
 97 Val Arg Lys Glu Gly Phe Leu Gly Ile Met Val Ile Tyr Gly Lys His
 98 370 375 380
 100 Ala Glu Val Gly Ser Gly Ile Phe Ile Ser Asp Leu Arg Glu Gly Ser
 101 385 390 395 400
 103 Asn Ala Glu Leu Ala Gly Val Lys Val Gly Asp Met Leu Leu Ala Val
 104 405 410 415
 106 Asn Gln Asp Val Thr Leu Glu Ser Asn Tyr Asp Asp Ala Thr Gly Leu
 107 420 425 430
 109 Leu Lys Arg Ala Glu Gly Val Val Thr Met Ile Leu Leu Thr Leu Lys
 110 435 440 445
 112 Ser Glu Glu Ala Ile Lys Ala Glu Lys Ala Ala Glu Glu Lys Lys
 113 450 455 460
 115 Glu Glu Ala Lys Lys Glu Glu Lys Pro Gln Glu Pro Ala Thr Ala
 116 465 470 475 480
 118 Glu Ile Lys Pro Asn Lys Lys Ile Leu Ile Glu Leu Lys Val Glu Lys
 119 485 490 495
 121 Lys Pro Met Gly Cys His Arg Leu Arg Arg Gln Lys Gln Pro Cys His
 122 500 505 510
 124 Asp Trp Leu Cys Asn His Pro Arg Leu Ser Gly Gly Gln Val Ala Ala
 125 515 520 525
 127 Asp Lys Arg Leu Lys Ile Phe Asp His Ile Cys Asp Ile Asn Gly Thr
 128 530 535 540
 130 Pro Ile His Val Gly Ser Met Thr Thr Leu Lys Val His Gln Leu Phe
 131 545 550 555 560
 133 His Thr Thr Tyr Glu Lys Ala Val Thr Leu Thr Val Phe Arg Ala Asp
 134 565 570 575
 136 Pro Pro Glu Leu Glu Lys Phe Asn Val Asp Leu Met Lys Lys Ala Gly
 137 580 585 590
 139 Lys Glu Leu Gly Leu Ser Leu Ser Pro Asn Glu Ile Gly Cys Thr Ile
 140 595 600 605
 142 Ala Asp Leu Ile Gln Gly Gln Tyr Pro Glu Ile Asp Ser Lys Leu Gln
 143 610 615 620
 145 Arg Gly Asp Ile Ile Thr Lys Phe Asn Gly Asp Ala Leu Glu Gly Leu

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146 625          630          635          640
148 Pro Phe Gln Val Cys Tyr Ala Leu Phe Lys Gly Ala Asn Gly Lys Val
149           645          650          655
151 Ser Met Glu Val Thr Arg Pro Lys Pro Thr Leu Arg Thr Glu Ala Pro
152           660          665          670
154 Lys Ala
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 2059
159 <212> TYPE: DNA
160 <213> ORGANISM: Drosophila melanogaster
162 <400> SEQUENCE: 2
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165 qacaagacggc gcaagaaggc cttccggatc tgcatagtgc qcggcgaggt gaaaggatttcg      120
167 cccaaaccca agacaacccgg catcttcatc aaggggcatg tgcccgacag tccccgcgc      180
169 ctgtgtggtc gcctaaaggt tggcgatecg atccctctgc tcaacggaaa ggatgtgcgc      240
171 aactccacccg aacaggcggt catcgatctc atcaaggagg cggaacctaa gatcgagctg      300
173 gagattcaqg ccttcgacaa gagcgtatgag caqccggcc aytcaqatcc gcccggacat      360
175 ggctacatgc aggccaagaa caaggatcaat cggaggatc ccaccaacaa caatgcgtcc      420
177 ggaggtcagg gaatggggca ayytccgggt cagggtcagg gaatggctgg catgaacccgg      480
179 caqcaatcqg tgcagaagcg qaataccaca ttccacggct ctagtgcqtc gaaqccataq      540
181 aactaccccg acgaggatga cgaggacacc cgggacatgaa ccgggtcgat tcgcacggag      600
183 ggggttatg agatcgatcg agccctccqcc ggttaatttgc aacttaataa gcaggaaaaag      660
185 gatcgacaca aggaggcggaa agatgaattt ggctacacatc tggctaaatg caacaaggcg      720
187 tacaacatcg tgaaggatct tgcgcaggatc gaggttcagg gggacgcccgg caagccactg      780
189 qqactccgcac tgcgtggcca caaqgaccygc cagaayatgg cctgctttgt tgccgggtq      840
191 gatecccaacg gagcattggg cagcgtggac attaagccgg ggcacgagat cgtcgagggtc      900
193 aacggcaatg tgcctaagaa tgcgtgccac ttgaacggctt ccggcgtgtt caagagcggt      960
195 gatggggata agctcgatg gatcaccccg cgaecgcaayc ccaacatgaa gggcatgtgc      1020
197 gtcaagccca tcaaaaagtgc tcccacccygc tctgtatgaa ctaagtttat cticgaccag      1080
199 ttcccaagg cgcgcacccgtt gcaaggatgc aaggagggtt cttggccatc atggatctc      1140
201 atggcaagca cgcgtggatg ggcagtgccat ttccatctc ggatctgaga gagggatcga      1200
203 atgcgcgatgtt ggcgggctg aaagtggcg acatgtgtgtt ggcgcgttaat caggatgtaa      1260
205 cactggatc caactacatg gatcgactcg gactgtgtt acgtggccgg ggcgtatgtt      1320
207 ccatgtatc attgactctc aagagcgagg aggcataaa ggcgtgagaag gcaagcggaag      1380
209 aaaaaaaaaaa ggaggaggcc aagaaagagg agggaaagcc acaggaaaccc gccacacccg      1440
211 agatcaaycc gaacaaaaaaat atactcattt gatgttggatg gggaaagaaag ccaatggcg      1500
213 tcacgtctg cggcgcgcaag aacaaccatg tcacgactgg ctgtgtatac acccacgtt      1560
215 atccggggggg acaatgtgc gcccggccaa gcttcacatg ctgtgttgcatttgcata      1620
217 taaatggatc gccaatccac gtgggatcca tgcacgacact gaagggtccat cagtatttcc      1680
219 acacacatac cggaaaggcg gtcacccctaa cgtgtttccg cgtgtatctc cccggactgg      1740
221 aaaagttaa cgttgacctt atqaaaaaaat cggcaagggc gtcgggctg tgcgtgttgc      1800
223 ccaacgaaat tggatgcacc atcgccgact tggatcaagg acaataccgg gagattgaca      1860
225 gcaaaactgcgca ggcggccgat attatccacca attaatggc gatgccttgg agggtcttcc      1920
227 gttccagggtg tgcgtacgtt tggatcaagg aaccaacggc aagggtatcga tggaaagtgc      1980
229 acgacccaaag cccactctac gtacggggc acccaacggcc tagagacgtt cctcatttctc      2040
231 ctctccgtat cgaaggatgtt      2059
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 93
236 <212> TYPE: PRT

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Input Set : A:\sequence
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237 <213> ORGANISM: artificial
 239 <220> FEATURE:
 240 <223> OTHER INFORMATION: PSD-1
 242 <400> SEQUENCE: 3
 244 Met Glu Tyr Glu Glu Ile Thr Leu Glu Arg Gly Asn Ser Gly Leu Gly
 245 1 5 10 15
 247 Phe Ser Ile Ala Gly Gly Thr Asp Asn Pro His Ile Gly Asp Asp Pro
 248 20 25 30
 250 Ser Ile Phe Ile Thr Lys Ile Ile Pro Gly Gly Ala Ala Ala Gln Asp
 251 35 40 45
 253 Gly Arg Leu Arg Val Asn Asp Ser Ile Leu Phe Val Asn Glu Val Asp
 254 50 55 60
 256 Val Arg Glu Val Thr His Ser Ala Ala Val Glu Ala Leu Lys Glu Ala
 257 65 70 75 80
 259 Gly Ser Ile Val Arg Leu Tyr Val Met Arg Arg Lys Pro
 260 85 90
 262 <210> SEQ ID NO: 4
 263 <211> LENGTH: 93
 264 <212> TYPE: PRT
 265 <213> ORGANISM: Artificial
 267 <220> FEATURE:
 268 <223> OTHER INFORMATION: PSD95-2
 270 <400> SEQUENCE: 4
 272 Glu Lys Val Met Glu Ile Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly
 273 1 5 10 15
 275 Phe Ser Ile Ala Gly Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn
 276 20 25 30
 278 Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly Gly Ala Ala His Lys Asp
 279 35 40 45
 281 Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu Ala Val Asn Ser Val Gly
 282 50 55 60
 284 Leu Glu Asp Val Met His Glu Asp Ala Val Ala Ala Leu Lys Asn Thr
 285 65 70 75 80
 287 Tyr Asp Val Val Tyr Leu Lys Val Ala Lys Pro Ser Asn
 288 85 90
 290 <210> SEQ ID NO: 5
 291 <211> LENGTH: 87
 292 <212> TYPE: PRT
 293 <213> ORGANISM: artificial
 295 <220> FEATURE:
 296 <223> OTHER INFORMATION: PSD95-3
 298 <400> SEQUENCE: 5
 300 Arg Glu Pro Arg Arg Ile Val Ile His Arg Gly Ser Thr Gly Leu Gly
 301 1 5 10 15
 303 Phe Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe
 304 20 25 30
 306 Ile Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly
 307 35 40 45
 309 Asp Gln Ile Leu Ser Val Asn Gly Val Asp Leu Arg Asn Ala Ser His

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310      50          55          60
312 Glu Gln Ala Ala Ile Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile
313 65          70          75          80
315 Ile Ala Gln Tyr Lys Pro Glu
316          85
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 87
320 <212> TYPE: PRT
321 <213> ORGANISM: artificial
323 <220> FEATURE:
324 <223> OTHER INFORMATION: dlg-3
326 <400> SEQUENCE: 6
328 Arg Glu Pro Arg Thr Ile Thr Ile Gln Lys Gly Pro Gln Gly Leu Gly
329 1          5          10          15
331 Phe Asn Ile Val Gly Gly Glu Asp Gly Gln Gly Ile Tyr Val Ser Phe
332          20          25          30
334 Ile Leu Ala Gly Gly Pro Ala Asp Leu Gly Ser Glu Leu Lys Arg Gly
335          35          40          45
337 Asp Gln Leu Leu Ser Val Asn Asn Val Asn Leu Thr His Ala Thr His
338          50          55          60
340 Glu Glu Ala Ala Gln Ala Leu Lys Thr Ser Gly Gly Val Val Thr Leu
341 65          70          75          80
343 Leu Ala Gln Tyr Arg Pro Glu
344          85
346 <210> SEQ ID NO: 7
347 <211> LENGTH: 88
348 <212> TYPE: PRT
349 <213> ORGANISM: artificial
351 <220> FEATURE:
352 <223> OTHER INFORMATION: nnos
354 <400> SEQUENCE: 7
356 Pro Asn Val Ile Ser Val Arg Leu Phe Lys Arg Lys Val Gly Gly Leu
357 1          5          10          15
359 Gly Phe Leu Val Lys Glu Arg Val Ser Lys Pro Pro Val Ile Ile Ser
360          20          25          30
362 Asp Leu Ile Arg Gly Gly Ala Ala Glu Gln Ser Gly Leu Ile Gln Ala
363          35          40          45
365 Gly Asp Ile Ile Leu Ala Val Asn Asp Arg Pro Leu Val Asp Leu Ser
366          50          55          60
368 Tyr Asp Ser Ala Leu Glu Val Leu Arg Gly Ile Ala Ser Glu Thr His
369 65          70          75          80
371 Val Val Leu Ile Leu Arg Gly Pro
372          85
374 <210> SEQ ID NO: 8
375 <211> LENGTH: 88
376 <212> TYPE: PRT
377 <213> ORGANISM: artificial
379 <220> FEATURE:
380 <223> OTHER INFORMATION: inad-3

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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/462,517

DATE: 11/21/2000
TIME: 11:52:47

Input Set : A:\sequence
Output Set: N:\CRF3\11212000\I462517.raw

L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

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